



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/688, 286 A

Source: OIPE

Date Processed by STIC: 7/5/2001

RECEIVED
JUL 31 2001
TECH CENTER 1600 2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence

RECEIVED

JUL 31 2001

TECH CENTER 1600 2900

Raw Sequence Listing Error Summary

ERROR DETECTED**SUGGESTED CORRECTION**SERIAL NUMBER: 09/688, 284 A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3, this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please **ensure your subsequent submission is saved in ASCII text.**
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES." response to **include** the skipped sequences.
- 8 Skipped Sequences (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
- 10 ✓ Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file.

OIPE

RAW SEQUENCE LISTING

DATE: 07/05/2001

PATENT APPLICATION: US/09/688,286A

TIME: 10:37:06

Input Set : A:\SEQUENCE.asc

Output Set: N:\CRF3\07052001\I688286A.raw

4 <110> APPLICANT: Willson, Tracy
 5 Nicola, Nicos A.
 6 Hilton, Douglas J.
 7 Metcalf, Donald
 8 Zhang, Jian G.
 10 <120> TITLE OF INVENTION: NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES
 11 ENCODING SAME
 13 <130> FILE REFERENCE: Davies Collison Cave
 15 <140> CURRENT APPLICATION NUMBER: 09/688,286A
 C--> 16 <141> CURRENT FILING DATE: 2001-06-20
 18 <150> PRIOR APPLICATION NUMBER: 09/051,843
 19 <151> PRIOR FILING DATE: 1998-06-29
 21 <160> NUMBER OF SEQ ID NOS: 11
 23 <170> SOFTWARE: PatentIn Ver. 2.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 1383
 27 <212> TYPE: DNA
 28 <213> ORGANISM: (nuc. & predicted a.a. seq. of mNR4)
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (61)..(1338)
 34 <220> FEATURE:
 35 <221> NAME/KEY: unsure
 36 <222> LOCATION: (121)
 37 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
 38 region
 40 <220> FEATURE:
 41 <221> NAME/KEY: unsure
 42 <222> LOCATION: (122)
 43 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
 44 region
 46 <220> FEATURE:
 47 <221> NAME/KEY: unsure
 48 <222> LOCATION: (123)
 49 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
 50 region
 52 <220> FEATURE:
 53 <221> NAME/KEY: unsure
 54 <222> LOCATION: (640)
 55 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
 56 region
 58 <220> FEATURE:
 59 <221> NAME/KEY: unsure

Does Not Comply
Corrected Diskette Needed
see pgs 5

see item #10 on
Error Summary Sheet.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/688,286A

DATE: 07/05/2001

TIME: 10:37:06

Input Set : A:\SEQUENCE.asc

Output Set: N:\CRF3\07052001\I688286A.raw

```

65 <221> NAME/KEY: unsure
66 <222> LOCATION: (642)
67 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
68     region
70 <400> SEQUENCE: 1
71 tgaaaagata gaataaatgg cctcgtgccg aattcggcac gagccgaggc gagggcctgc 60
74 atg gcg cgg cca gcg ctg ctg ggc gag ctg ttg gtg ctg cta ctg tgg 108
75 Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Leu Val Leu Leu Leu Trp
76 1 5 10 15
W--> 78 acc gcc acc gtg nnn ggc caa gtt gcc gcg gcc aca gaa gtt cag cca 156
W--> 79 Thr Ala Thr Val Xaa Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro
80 20 25 30
82 cct gtg acg aat ttg agc gtc tct gtc gaa aat ctc tgc acg ata ata 204
83 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile
84 35 40 45
86 tgg acg tgg agt cct cct gaa gga gcc agt cca aat tgc act ctc aga 252
87 Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg
88 50 55 60
90 tat ttt agt cac ttt gat gac caa cag gat aag aaa att gct cca gaa 300
91 Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu
92 65 70 75 80
94 act cat cgt aaa gag gaa tta ccc ctg gat gag aaa atc tgt ctg cag 348
95 Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln
96 85 90 95
98 gtg ggc tct cag tgt agt gcc aat gaa agt gag aag cct agc cct ttg 396
99 Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu
100 100 105 110
102 gtg aaa aag tgc atc tca ccc cct gaa ggt gat cct gag tcc gct gtg 444
103 Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
104 115 120 125
106 act gag ctc aag tgc att tgg cat aac ctg agc tat atg aag tgt tcc 492
107 Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
108 130 135 140
110 tgg ctc cct gga agg aat aca agc cct gac aca cac tat act ctg tac 540
111 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr
112 145 150 155 160
114 tat tgg tac agc agc ctg gag aaa agt cgt caa tgt gaa aac atc tat 588
115 Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr
116 165 170 175
118 aga gaa ggt caa cac att gct tgt tcc ttt aaa ttg act aaa gtg gaa 636
119 Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu
120 180 185 190
W--> 122 cct nnn agt ttt gaa cat cag aac gtt caa ata atg gtc aag gat aat 684
W--> 123 Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn
124 195 200 205
126 gct ggg aaa att agg cca tcc tgc aaa ata gtg tct tta act tcc tat 732
127 Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/688,286A

DATE: 07/05/2001

TIME: 10:37:06

Input Set : A:\SEQUENCE.asc

Output Set: N:\CRF3\07052001\I688286A.raw

```

131 Val Lys Pro Asp Pro Pro His Ile Lys His Leu Leu Lys Asn Gly
132 225 230 235 240
134 gcc tta tta gtg cag tgg aag aat cca caa aat ttt aga agc aga tgc 828
135 Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys
136 245 250 255
138 tta act tat gaa gtg gag gtc aat aat act caa acc gac cga cat aat 876
139 Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn
140 260 265 270
142 att tta gag gtt gaa gag gac aaa tgc cag aat tcc gaa tct gat aga 924
143 Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg
144 275 280 285
146 aac atg gag ggt aca agt tgt ttc caa ctc cct ggt gtt ctt gcc gac 972
147 Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp
148 290 295 300
150 gct gtc tac aca gtc aga gta aga gtc aaa aca aac aag tta tgc ttt 1020
151 Ala Val Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe
152 305 310 315 320
154 gat gac aac aaa ctg tgg agt gat tgg agt gaa gca cag agt ata ggt 1068
155 Asp Asp Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly
156 325 330 335
158 aag gag caa aac tcc acc ttc tac acc acc atg tta ctc acc att cca 1116
159 Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro
160 340 345 350
162 gtc ttt gtc gca gtg gca gtc ata atc ctc ctt ttt tac ctg aaa agg 1164
163 Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg
164 355 360 365
166 ctt aag atc att ata ttt cct cca att cct gat cct ggc aag att ttt 1212
167 Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
168 370 375 380
170 aaa gaa atg ttt gga gac cag aat gat gat acc ctg cac tgg aag aag 1260
171 Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
172 385 390 395 400
174 tat gac atc tat gag aaa caa tcc aaa gaa gaa acg gat tct gta gtg 1308
175 Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val
176 405 410 415
178 ctg ata gaa aac ctg aag aaa gca gct cct tgatggggag aagtgatttc 1358
179 Leu Ile Glu Asn Leu Lys Lys Ala Ala Pro
180 420 425
182 tttcttgcct tcaatgtgac cctgt 1383
186 <210> SEQ ID NO: 2
187 <211> LENGTH: 426
188 <212> TYPE: PRT
189 <213> ORGANISM: nuc. & predicted a.a. seq. of mNR4 ) see page 1
191 <220> FEATURE:
192 <221> NAME/KEY: unsure
193 <222> LOCATION: (21)
194 <223> OTHER INFORMATION: authors are unsure about the sequence assignment

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/688,286A

DATE: 07/05/2001

TIME: 10:37:06

Input Set : A:\SEQUENCE.asc

Output Set : N:\CRF3\07052001\I688286A.raw

198 <222> LOCATION: (194)

199 <223> OTHER INFORMATION: authors are unsure about the sequence assignment

201 <400> SEQUENCE: 2

202 Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Leu Val Leu Leu Leu Trp

203 1 5 10 15

W--> 205 Thr Ala Thr Val Xaa Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro

206 20 25 30

208 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile

209 35 40 45

211 Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg

212 50 55 60

214 Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu

215 65 70 75 80

217 Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln

218 85 90 95

220 Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu

221 100 105 110

223 Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val

224 115 120 125

226 Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser

227 130 135 140

229 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr

230 145 150 155 160

232 Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr

233 165 170 175

235 Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu

236 180 185 190

W--> 238 Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn

239 195 200 205

241 Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr

242 210 215 220

244 Val Lys Pro Asp Pro Pro His Ile Lys His Leu Leu Lys Asn Gly

245 225 230 235 240

247 Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys

248 245 250 255

250 Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn

251 260 265 270

253 Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg

254 275 280 285

256 Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp

257 290 295 300

259 Ala Val Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe

260 305 310 315 320

262 Asp Asp Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly

263 325 330 335

265 Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro

266 340 345 350

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/688,286A

DATE: 07/05/2001

TIME: 10:37:06

Input Set : A:\SEQUENCE.asc

Output Set: N:\CRF3\07052001\I688286A.raw

```

271 Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
272      370      375      380
274 Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
275 385      390      395      400
277 Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val
278      405      410      415
280 Leu Ile Glu Asn Leu Lys Lys Ala Ala Pro
281      420      425
284 <210> SEQ ID NO: 3
285 <211> LENGTH: 1383
286 <212> TYPE: DNA
287 <213> ORGANISM: Human IL-13 receptor alpha-chain
289 <220> FEATURE:
290 <221> NAME/KEY: CDS
291 <222> LOCATION: (61)..(1338)
293 <400> SEQUENCE: 3
294 gagtctaaca cggaccaagg agttaaacaac gtgcggccgg gttccgaggc gagaggctgc 60
297 atg gag tgg ccg gcg cgc ctc tgc ggg ctg tgg gcg ctg ctg ctc tgc 108
298 Met Glu Trp Pro Ala Arg Leu Cys Gly Leu Trp Ala Leu Leu Leu Cys
299 1      5      10      15
301 gcc ggc ggc ggg ggc ggg ggc ggg ggc gcg cct acg gaa act cag cca 156
302 Ala Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Thr Glu Thr Gln Pro
303      20      25      30
305 cct gtg aca aat ttg agt gtc tct gtt gaa aac ctc tgc aca gta ata 204
306 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile
307      35      40      45
309 tgg aca tgg aat cca ccc gag gga gcc agc tca aat tgt agt cta tgg 252
310 Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp
311 50      55      60
313 tat ttt agt cat ttt ggc gac aaa caa gat aag aaa ata gct ccg gaa 300
314 Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu
315 65      70      75      80
317 act cgt cgt tca ata gaa gta ccc ctg aat gag agg att tgt ctg caa 348
318 Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln
319      85      90      95
321 gtg ggg tcc cag tgt agc acc aat gag agt gag aag cct agc att ttg 396
322 Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu
323      100      105      110
325 qtt gaa aaa tgc atc tca ccc cca gaa qgt gat cct gaq tct gct gtg 444
326 Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
327      115      120      125
329 act gag ctt caa tgc att tgg cac aac ctg agc tac atg aag tgt tct 492
330 Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
331      130      135      140
333 tgg ctc cct gga agg aat acc aqt ccc gac act aac tat act ctc tac 540
334 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr
335 145      150      155      160
337 tat tgg gaa ggc ggt gta gaa ggt ggt ggt ggt ggt ggt ggt ggt ggt

```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/688,286A

DATE: 07/05/2001

TIME: 10:37:07

Input Set : A:\SEQUENCE.asc

Output Set: N:\CRF3\07052001\I688286A.raw

L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:78 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:79 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:123 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:238 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:551 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:571 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:589 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11